

SEQUENCE LISTING

- (1) GENERAL INFORMATION
- (i) APPLICANT: DONNELLY, JOHN J. DWARKI, VARAVANI J. LIU, MARGARET A. MONTGOMERY, DONNA L. PARKER, SUEZANNE E. SHIVER, JOHN W. ULMER, JEFFREY B.
- (ii) TITLE OF THE INVENTION: NUCLEIC ACID PHARMACEUTICALS -INFLUENZA MATRIX
- (iii) NUMBER OF SEQUENCES: 64
- (iv) CORRESPONDENCE ADDRESS:

 (A) ADDRESSEE: J. MARK HAND MERCK & CO., INC.

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 - (C) CITY: RAHWAY
 - (D) STATE: NJ

 - (E) COUNTRY: USA (F) ZIP: 07065-0907
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 1.5
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 09/835,694
 - (B) FILING DATE: 16-April-2001
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/461,268
 - (B) FILING DATE: 05-June-1995
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: PCT/US94/02751
 - (B) FILING DATE: 14-March-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/089,985
 - (B) FILING DATE: 08-July-1993
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/032,383
 - (B) FILING DATE: 18-March-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: HAND, J. MARK
 - (B) REGISTRATION NUMBER: 36,545
 - (C) REFERENCE/DOCKET NUMBER: 18972PCA
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(2) INFORMATION FOR SEQ ID NO:1:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:	
GTGTGCACCT CAAGCTGG	18
(2) INFORMATION FOR SEQ ID NO:2:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:	
CCCTTTGAGA ATGTTGCACA TTC	23
(2) INFORMATION FOR SEQ ID NO:3:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:	
GGTACAAGAT CTACCATGCT TCTAACCGAG GTC	33
(2) INFORMATION FOR SEQ ID NO:4:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC	36
(2) INFORMATION FOR SEQ ID NO:5:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:	
CTATATAAGC AGAGCTCGTT TAG	23
(2) INFORMATION FOR SEQ ID NO:6:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:	
GTAGCAAAGA TCTAAGGACG GTGACTGCAG	30
(2) INFORMATION FOR SEQ ID NO:7:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA(iii) HYPOTHETICAL: NO(iv) ANTISENSE: NO(v) FRAGMENT TYPE:(vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:	

(2) INFORMATION FOR SEQ ID NO:8:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:	
GTGCGAGCCC AATCTCCACG CTCATTTCA GACACATAC	39
(2) INFORMATION FOR SEQ ID NO:9:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 9 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: peptide (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: None (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
Thr Tyr Gln Arg Thr Arg Ala Leu Val 1 5	
(2) INFORMATION FOR SEQ ID NO:10:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 4432 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:	
TCGCGCGTTT CGGTGATGAC GGTGAAAACC TCTGACACAT GCAGCTCCCG GAGACGGTCA CAGCTTGTCT GTAAGCGGAT GCCGGAGCA GACAAGCCCG TCAGGGGCGC TCAGCGGGTG TCGGGGGTG CTTAACTATG CGGCATCAGA GCAGATTGTA CTGAGAGTGC ACCATATGCG GTGTAAAATA CCGCACAGAT GCGTAAGGAG AAAATACCGC ATCAGATTGG CTATTGGCCA TTGCATACGT TGTATCCATA TCATAATATG TACATTTATA TTGGCTCATG TCCAACATTA CCGCCATGTT GACATTGATT ATTGACTAGT TATTAATAGT AATCAATTAC	120 180 240 300 360

GTATGTGTCT GAAAATGAGC GTGGAGATTG GGCTCGCAC

39

GGGGTCATTA	GTTCATAGCC	CATATATGGA	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	420
CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	480
CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGAGTATT	TACGGTAAAC	540
TCCCCACTTC	CCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCCTA	TTGACGTCAA	600
TOCCOMO A A	TCCCCCCCCT	GGCATTATGC	CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	660
TGACGG I AAA	AMCMACCMAM	TAGTCATCGC	TATTACCATC	CTCATCCCCT	TTTGGCAGTA	720
TTGGCAGTAC	ATCTACGTAT	GGTTTGACTC	ACCCCCAMM	CCAACTCCCCC	ACCCCATTCA	780
CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATTT	CCAAGICICC	ACCCCA11GA	
CGTCAATGGG	AGTTTGTTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA	840
CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	900
AGCTCGTTTA	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCGTGCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGGC	1080
ጥጥርጥጥልጥርር <u>እ</u>	TGCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCCGCT	TCCTCATGTT	1140
ATACCTCATC	$CT\Delta T\Delta CCTT\Delta$	GCCTATAGGT	GTGGGTTATT	GACCATTATT	GACCACTCCC	1200
CHAMMCCMCA	CCATACTTC	CATTACTAAT	CCATAACATG	CCTCTTTCCC		1260
CTATIGGIGA	CGATACTIC	CACTGTCCTT	CACACACTCA	CACCCACTCT	$CT\Delta TTTTT\Delta C$	1320
TTATTGGCTA	TATGCCAATA	ATTTACAAAT	TO A CAMAMAC	AACACCACCC	TCCCCACTCC	1380
AGGATGGGGT	CTCATTTATT	ATTTACAAAT	TCACATATAC	AMCACCACCG	COMOMMOCOCO	1440
		AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCCGG	
ACATGGGCTC	TTCTCCGGTA	GCGGCGGAGC		GAGCCCTGCT		1500
CAGCGACTCA	TGGTCGCTCG	GCAGCTCCTT	GCTCCTAACA	GTGGAGGCCA	GACTTAGGCA	1560
CAGCACGATG	CCCACCACCA	CCAGTGTGCC	GCACAAGGCC	GTGGCGGTAG	GGTATGTGTC	1620
TGAAAATGAG	CTCGGGGAGC	GGGCTTGCAC	CGCTGACGCA	TTTGGAAGAC	TTAAGGCAGC	1680
GGCAGAAGAA	GATGCAGGCA	GCTGAGTTGT	TGTGTTCTGA	TAAGAGTCAG	AGGTAACTCC	1740
CCTTCCCCTC	CTCTTAACGG	TGGAGGGCAG	TGTAGTCTGA	GCAGTACTCG	TTGCTGCCGC	1800
CCCCCCCACC	ACACATA ATA	GCTGACAGAC	TAACAGACTG	TTCCTTTCCA	TGGGTCTTTT	1860
GCGCGCCACC	AGACATAATA	TCTGCTGTGC	CMMCMACMMC	CCACCCATCT	CTTCTTTCCC	1920
CTGCAGTCAC	CGTCCTTAGA	TCTGCTGTGC	CTICIAGIIG	CCAGCCAICI	TCCTA ATA A A	1980
CCTCCCCCGT	GCCTTCCTTG	ACCCTGGAAG	GIGCCACICC	CACTGICCII	COMCOCOMCC	2040
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCATTC	TATTCTGGGG	GGTGGGGTGG	2100
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	GCATGCTGGG	GATGCGGTGG	
GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	AGAAAGAAGC	2160
AGGCACATCC	CCTTCTCTGT	GACACACCCT	GTCCACGCCC	CTGGTTCTTA	GTTCCAGCCC	2220
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CTCCGCCTTC	AATCCCACCC	GCTAAAGTAC	2280
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGTGG	2340
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2400
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	TGACTCGCTG	2460
CGCTCGGTCG	TTCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2580
ACCAACCCTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2640
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2700
CAICACAAAA	CCCCTCCAAC	CTCCCTCGTG	CCCTCTCCTC	TTCCGACCCT	GCCGCTTACC	2760
CAGGCGIIIC	CCCCIGGAAG	CCCTTCGGGA	ACCCTCCCC	ጥጥጥርጥርልልጥር	CTCACGCTGT	2820
CGATACCTGT	CCGCCTTTCT	GGTCGTTCGC	TOCOTOGCOC	CCTCTCTCTCCA	CCAACCCCCC	2880
AGGTATCTCA	ACCCCTGIA	GGICGIICGC	A A CONTROCTOR	MUCA CUCCA A	CCCGGTAAGA	2940
GTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACIAICGIC	TIGAGICCAA	CACCUATOR	3000
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	COMPAGE	GAGGTATGTA	3060
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	3180
CGCAGAAAAA	AAGGATCTCA	AGAAGATCCT	TTGATCTTTT	CTACGGGGTC	TGACGCTCAG	3240
TGGAACGAAA	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	TATCAAAAAG	GATCTTCACC	3300
TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT	AAAGTATATA	TGAGTAAACT	3360
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTGTCTATTT	3420
CGTTCATCCA	TAGTTGCCTG	ACTCCCCGTC	GTGTAGATAA	CTACGATACG	GGAGGGCTTA	3480
CCATCTGGCC	CCAGTGCTGC	AATGATACCG	CGAGACCCAC	GCTCACCGGC	TCCAGATTTA	3540
TCACCAATAA	ACCAGCCAGC	CGGAAGGGCC	GAGCGCAGAA	GTGGTCCTGC	AACTTTATCC	3600
CCCTCCATCC	ΑСΤΌΤΑΤΤΑΑ	TTGTTGCCGG	GAAGCTAGAG	TAAGTAGTTC	GCCAGTTAAT	3660
ACTIOCATOC A	∆ ርርጥጥርጥጥር ር	CATTCCTACA	GGCATCGTGG	TGTCACGCTC	GTCGTTTGGT	3720
VACCCAMACY W	#CACC#CCC	<u> </u>	TCAACCCCAC	TTACATGATC	CCCCATGTTG	3780
MCCAAAAAAA	TCVGCTCCQQ		CCCVACCAVA	TCACAACTA	GTTGGCCGCA	3840
TGCAAAAAAG	CGGTTAGCTC	CITCGGICCI	CCGTTCGTIG		GCCATCCGTA	3900
GTGTTATCAC	TCATGGTTAT	GGCAGCACTG	ACCARACTOR	TIACIGICAL	GCCAICCGIA	3960
AGATGCTTTT	CTGTGACTGG	TGAGTACTCA	ACCAAGTCAT	TCTGAGAATA	GTGTATGCGG	4020
CGACCGAGTT	GCTCTTGCCC	GGCGTCAATA	CGGGATAATA	A A COCCOCCACA	TAGCAGAACT	4020
TTAAAAGTGC	TCATCATTGG	AAAACGTTCT	TCGGGGCGAA	AACTUTUAAG	GATCTTACCG	4000

СТСТТСАСАТ	CCAGTTCGAT	GTAACCCACT	CGTGCACCCA	ACTGATCTTC	AGCATCTTTT	4140
ACTTTCACCA	GCGTTTCTGG	GTGAGCAAAA	ACAGGAAGGC	AAAATGCCGC	AAAAAAGGGA	4200
ATAAGGGCGA	CACGGAAATG	TTGAATACTC	ATACTCTTCC	TTTTTCAATA	TTATTGAAGC	4260
ATTTATCAGG	GTTATTGTCT	CATGAGCGGA	TACATATTTG	AATGTATTTA	GAAAAATAAA	4320
CAAATAGGGG	TTCCGCGCAC	ATTTCCCCGA	AAAGTGCCAC	CTGACGTCTA	AGAAACCATT	4380
ATTATCATGA	CATTAACCTA	TAAAAATAGG	CGTATCACGA	GGCCCTTTCG	TC	4432

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2196 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO

- (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATTGGCTATT	GGCCATTGCA	TACGTTGTAT	CCATATCATA	ATATGTACAT	TTATATTGGC	60
			TGATTATTGA			120
		TAGCCCATAT	ATGGAGTTCC			180
	CTGGCTGACC	GCCCAACGAC	CCCCGCCCAT			240
	TAACGCCAAT	AGGGACTTTC	CATTGACGTC			300
	ACTTGGCAGT	ACATCAAGTG	TATCATATGC			360
GTCAATGACG	GTAAATGGCC	CGCCTGGCAT	TATGCCCAGT	ACATGACCTT		420
CCTACTTGGC	AGTACATCTA	CGTATTAGTC	ATCGCTATTA			480
CAGTACATCA	ATGGGCGTGG	ATAGCGGTTT	GACTCACGGG	-		540
ATTGACGTCA	ATGGGAGTTT	GTTTTGGCAC	CAAAATCAAC	GGGACTTTCC		600
AACAACTCCG	CCCCATTGAC	GCAAATGGGC	GGTAGGCGTG			660
AGCAGAGCTC	GTTTAGTGAA	CCGTCAGATC	GCCTGGAGAC			720
	GACACCGGGA	CCGATCCAGC	CTCCGCGGCC			780
CGGATTCCCC	GTGCCAAGAG	TGACGTAAGT	ACCGCCTATA			840
TTGGCTTCTT	ATGCATGCTA	TACTGTTTTT	GGCTTGGGGT		••••	900
ATGTTATAGG	TGATGGTATA	GCTTAGCCTA	TAGGTGTGGG			960
CTCCCCTATT	GGTGACGATA	CTTTCCATTA				1020
TCTCTTTATT	GGCTATATGC	CAATACACTG				1080
TTTACAGGAT	GGGGTCTCAT	TTATTATTTA				1140
AGTGCCCGCA	GTTTTTATTA	AACATAACGT				1200
TCCGGACATG	GGCTCTTCTC	CGGTAGCGGC	GGAGCTTCTA			1260
GCCTCCAGCG	ACTCATGGTC	GCTCGGCAGC	TCCTTGCTCC			1320
AGGCACAGCA	CGATGCCCAC	CACCACCAGT				1380
						1440
GCAGCGGCAG	AAGAAGATGC	AGGCAGCTGA				1500
ACTCCCGTTG	CGGTGCTGTT	AACGGTGGAG				1560
GCCGCGCGCG	CCACCAGACA	TAATAGCTGA	CAGACTAACA			1620
CTTTTCTGCA	GTCACCGTCC	TTAGATCTGC	TGTGCCTTCT			1680
TTGCCCCTCC	CCCGTGCCTT	CCTTGACCCT	GGAAGGTGCC			1740
ATAAAATGAG	GAAATTGCAT	CGCATTGTCT	GAGTAGGTGT			1800
GGTGGGGCAG	CACAGCAAGG	GGGAGGATTG				1860
GGTGGGCTCT	ATGGGTACCC	AGGTGCTGAA				1920
GAAGCAGGCA	CATCCCCTTC	TCTGTGACAC	ACCCTGTCCA			1980
AGCCCCACTC	ATAGGACACT					2040
AGTACTTGGA	GCGGTCTCTC	CCTCCCTCAT	CAGCCCACCA			2100
AGTGGGAAGA				AGGGAGAGAA	AATGCCTCCA	2160
ACATGTGAGG	AAGTAATGAG	AGAAATCATA	GAATTC			2196
	TCATGTCCAA ATTACGGGGT AATGGCCCGC GTTCCCATAG TAAACTGCCC GTCAATGACG CCTACTTGGC CAGTACATCA AACACTCCG AGCAGAGCTC CTCCATAGAA CGGATTCCCC TTGGCTTCTT ATGTTATAGG CTCCCTATT TCTCTTTATT TTTACAGGAT AGGGCACAGCA AGCAGCGCAG AGGCACAGCA GCTCCCGTTG GCTCCCGTTG GCTCCCGCATG GCCTCCAGCG AGGCACAGCA GCGCGCGCGC ATTACATAAATGAG GCTGCCGCC ATTACATACACACA GCAGGGCACACACACACACACACACACACACA	TCATGTCCAA ATTACCGCC ATTACGGGGT CATTAGTTCA AATGGCCCGC GTTCCCATAG TAACGCCAAT TAACTGCCC GTCAATGACG GTAAATGGCC GTCAATGACG CCTACTTGGC CCTACTTGGC AGTACATCA ATGGGCGTGG ATTGACGTCA ATGGGAGTTT AACACTCCG CCCCATTGAC AGCAGAGCTC CTCCATAGAA CGCCAAGAG CGGATTCCCC TTGCCTATT ATGCATGCTA ATGTTATAGG CTCCCTATT CTCTTTATT TTTACAGGAT TCTCTTTATT TTTACAGGAT GGCTCTCTAT AGTGCCCCA GTGTCTCAT AGTGCCCCA GTGTCTGAA ATGAGCTCAT AGTGCCCCA GTGTCTGAAA ATGAGCTCG ACTCCCGTTG CCCGCGCGCG CCACCAGACA CTTTTCTGCA GCACCGCA CTTTTCTGCA CCACCAGACA CCACCAGCA CTTTTCTGCA CCACCAGCA CTTTTCTGCA CCACCAGCA CTTTTCTGCA CCACCAGCA CAAGCAAGG CAAGCAAGCA CAAGCAAG	TCATGTCCAA CATTACCGCC ATGTTGACAT ATTACGGGGT CATTAGTTCA TAGCCCATAT AATGGCCCGC CTGGCTGACC GCCCAACGAC GTTCCCATAG TAACGCCAAT AGGGACTTTC TAAACTGCCC ACTTGGCAGT ACATCAAGTG GTCAATGACG GTAAATGGCC CGCCTGGCAT AGTACATCA AGGGACTTTA CGTATTAGTC CAGTACATCA ATGGCGTGG ATAGCGGTTT ATTGACGTCA ATGGGAGTTT GTTTTGCCAC AGCAGAGCTC GTTTAGTGA CCGTCAGATC CTCCATAGAA GACACCGGGA CCGATCCAGC CGGATTCCCC GTGCCAAGAG CCGATCCAGC CTGCATAGAA GACACCGGGA CCGATCCAGC CTGCATAGAA GACACCGGGA CCGATCCAGC CTGCCTATT GGTGACGTA TACTGTTTT ATGTTATAGG TGATGGTAT TACTGTTTTT ATGTTATATG GGTGACGATA CTTTCCATTA TCTCTTTATT GGCTATATGC CAATACACTG TCCGGACATG GGCTCTCAT TATTATATATA AGTGCCCGCA GTTTTATTA AACATAACCTG GCTCCAGCG ACTCATGGTC CGGTAGCGGC GCTCCAGCG ACTCATGGTC CGGTAGCGGC GCAGCGCAG AAGAAGATGC CACCACCAGT GCAGCGCAG AAGAAGATGC CACCACCAGT GCAGCGCGCG CCACCAGACA TAATAGCTGA CTTTCTTCAGA ATGACCTCC CCCTGGCAGC ACTCCCGTTG CGGTGCTTT TATTATATCA GCCGCCCCCC CCCCAGACA TAATAGCTGA CTTTTCTGCA GTCACCGTC TTAGACCTC TTGCCCCTCC CCCGTGCCTT CCTTGACCCT ATAAAATGAG GAAATTGCAT CGCATTGTCT GGTGGGCAG AAGAAAGAGC GGGAGGATTG GGTGGGCAG AACACCAAGG GGGAGGATTG GGTGGGCAG AACACCAACG GGGAGGATTG GGTGGGCAG AACACCAACG GGGAGGATTG GGTGGGCAG AACACCAACC AGGTGCTGAA AGCCCCACTC ATAGGACAC AGGTGCTGAA AGCCCCACTC ATAGGACAC CATAGCTCAC AGCCCCACTC ATAGGACAC CATAGCTCAC AGCCCCACTC ATAGGACAC CATAGCTCAC AGCACCACCACACACACACACACACACACACACACA	TCATGTCCAA ATTACGGGT ATTACGGGGT AATGGCCCGC CTGCTGACC GTTCCCATAG TTAACGCCAAT AATGGCCCGC GTTCCCATAG TTAACGCCAAT TAAACTGCCC GTTAACTGCCC ACTTGGCAGT ACTTGGCAGT ACTTGGCAGT TAAACTGCCC GTAATTAGCC CTACTTGGC GTAAATGGCC CCCATCTAC GTCAATGACG GTAAATGGCC CCCATCTAC ATGGCGTGAC CCCATTGGC CCTACTTGC CAGTACATCA ATGGGCGTGG ATTAGCGCAT ATGGCGTCA ATGGGCGTGG CCCATTGAC CCCATTGAC CCCATTGAC CCCATTGAC CCCATTGAC CCCATTGAC CCCCATTGAC CCCATTGAC CCCCATTGAC CCCCATTGAC CCCATTGAC CCCCATTGAC CCCCATTGAC CCCCATTAGAC CCCCCATTAC CCCCATTAGAC CCCCCATTAC CCCCATTAC CCCCCATTAC CCCCCTATT CGCTCACC CTCCCCTAT CGCTCACCAC CTCCCCCTAT CCCCCTAT CCCCCATTAC CCCCCTAT CCCCCTAT CCCCCTAT CCCCCTAT CCCCCTAT CCCCCTAT CCCCCATTCC CCCATTCAC CCCCCCCATTC CCCCTCCCCCC CCCCCCCATT CCCCCCATC CCCCCCCC	TCATGTCCAA CATTACCGC ATTACCGCC ATTACTCCAA ATTACGGGGT CATTAGTTCA ATTACGGGGT CATTAGTTCA ATTGCCCATAT ATTGCCCCCCCCCTGCCTGCC GCCCACCACCA ATGGCCCCAT ATGGCCCCAT TAGCCCCATAT ATGCAGTCAA ATGGCCCCAT TAGCCCCATAT TAGCCCCATAT TAGCCCCATAT TAGCGCCCAT TAGCGCCCAT TAGCGCCAAT TAGCGCCCAT TAGCCCCAT TAGCGCCCAT TAGCGCCCC TCCATCTTGGC ATTAGCGCT TAGCGCCTT TAGCGCTT TAGCGCTT TAGCGCCCC TCCATGGC TTTAGTGAC TCCCCCATTGAC CCCCATTGAC CCGCCCAT CCCCCTATA CCCCCTATA CCCCCCTAT CCCCCTAT CCCCCCTAT CCCCCCTAT CCCCCCTAT CCCCCTAT CCCCCCTAT CCCCCTAT CCCCCCTAT CCCCCCTCC CCCCCCCC	TCATGTCCAA ATTACGGGG TCATTAGTTCA TAGCCCATA ATTACGGGGG CTGGCTGACC GCCCAACGAC GTCCCATAG TTACGCCCAT GTTCCCATAG TTACGCCAT ACTGCCATA GTTCCCATAG TTACGCCAT ACTGCCATA TAACGCCAAT AGGGACTTC CTACTTGC GTTCCCATAG TAACGCCAAT AGGGACTTC CATTGACGC ACTTGGCAGT TAACGCCAT TAACGCCAT TAACGCCAT TAACGCCAT TAACGCCAT TAACGCCAT TAACGCCAT TAACGCCAT TATCATATGC CAATAACTGC CGCTTGCATT CCTACTTGC CGTACATCA ATGGGACTT CCTACTTGC CAGTACATCA ATGGGACTT TGTTTTGCCAC AGTACATCA ATGGGACTT TGTTTGCCAC AGTACATCA ATGGGACTT TGTTTTGCCAC AGCACACCAC AGCACACCAC CCCCATTGAC CAAAATCAAC CCCCATTCAC CCCCATTGAC CAAAATCAAC CCCCATTCAC CCCCATTGAC CAAAATCAAC CCCCATTCAC CCCCATTGAC CAAAATCAAC CCCCATTGAC CAAAATCAAC CCCCATTCAC CCCCATTGAC CAAAATCAAC CCCCATTCAC CCCCATTGAC CAAAATCAAC CCCCCATTGAC CAAAATCAAC CCCCCATTGAC CAAAATCACA CCCCCATTGAC CAAAATCAAC CCCCCATTGAC CAAAATCAAC CCCCCATTGAC CAAAATCAAC CCCCCATTCAC CCCCCATTGAC CAAAATCAAC CCCCCATTCAC CCCCCATTGAC CCCCCATTGAC CAAAATCACAC CCCCCTATTAC CCCCCATTGAC CAAAATCACC CCCCTCATTC CTCCCATAGA CTCCCCCTATT CGTGACGATA CTTCCACAGAT CTTCCATAGAC CTCCCCTATT CGTGACGATA CTTCCATAGAC CTCCCCTATT CGTGACGATA CTTTCCATTA CTTACACCC CCGCCCTAT CGTGACGATA CTTTCCATTA CTTACACCC CCGCCCTAT CCCCCTATT CGTGACGATA CTTTCCATTA CTTACACCC CCGCCCTAT CCCCCTATT CCTCCATTATTACG CCCCCATTATAC CCCCCCATTCAC CCCCCTATT CCTCCATGCAC CCCCCATTCAC CCCCCATTCAC CCCCCTATT CCTCCATAGAC CCCCCCATTAC CCCCCATTAC CCCCCCATTCAC CCCCCATTCAC CCCCCATTCAC CCCCCCTATT CCTCCCCTAT CCTCCATTAC CCCCCCATTCAC CCCCCTATTCC CCTCCATTCT CCTCCATCAC CCCCCTATTCC CCTCCATTCT CCTCCATCAC CCCCCCTATT CCTCCATCAC CCCCCCTATT CCCCCCTATT CCTCCATCAC CCCCCCTCT CTTCCACCC CCCCTCCTCT CCTCCACCC CCCCTCCCCC CCCCTCCCCC CCCCTCCCCCC CCCCCTCCCCC CCCCTCCCCCC

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 71 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTAGA TAATCACTCA CTGAGTGACA TCAAAATCAT G	60 71
(2) INFORMATION FOR SEQ ID NO:13:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 117 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
ACCGTCCTTA GATCAGCTTG GCAAAAGCAG GCAAACCATT TGAATGGATG TCAATCCGAC CTTACTTTC TTAAAAGTGC CAGCACAAAA TGCTATAAGC ACAACTTTCC CTTATAC	60 117
(2) INFORMATION FOR SEQ ID NO:14:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 136 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both 	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
GTCACCGTCC TTAGATCAAT TCCAGCAAAA GCAGGGTGAC AAAAACATAA TGGATCCAAA CACTGTGTCA AGCTTTCAGG TAGATTGCTT TCTTTGGCAT GTCCGCAAAC GAGTTGCAGA CCAAGAACTA GGTGAT	60 120 136
(2) INFORMATION FOR SEQ ID NO:15:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 152 base pairs(B) TYPE: nucleic acid	

(C) STRANDEDNESS: double (D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
TCTGCAGTCA CCGTCCTTAG ATCAGCTTGG AGCAAAAGCA GGGGAAAATA AAAACAACCA AAATGAAGGC AAACCTACTG GTCCTGTTAA GTGCACTTGC AGCTGCAGAT GCAGACACAA TATGTATAGG CTACCATGCG AACAATTCAA CC	60 120 152
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 162 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both 	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	
TTTTCTGCAG TCACCGTCCT TAGATCCCGA ATTCCAGCAA AAGCAGGTCA ATTATATTCA ATATGGAAAG AATAAAAGAA CTAAGAAATC TAATGTCGCA GTCTGCCACC CCGGAGATAC TCACAAAAAC CACCGTGGAC CATATGGCCA TAATCAAGAA GT	60 120 162
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 122 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GTCACCGTCC TTAGATCTAC CATGAGTCTT CTAACCGAGG TCGAAACGTA CGTACTCTCT ATCATCCCGT CAGGCCCCCT CAAAGCCGAG ATCGCACAGA GACTTGAAGA GTTGACGGAA GA	60 120 122
(2) INFORMATION FOR SEQ ID NO:18:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 4864 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both	

- (ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

					a- a- aaaama-	C 0
TCGCGCGTTT	CGGTGATGAC	GGTGAAAACC	TCTGACACAT	GCAGCTCCCG	GAGACGGTCA	60
CAGCTTGTCT	GTAAGCGGAT	GCCGGGAGCA	GACAAGCCCG	TCAGGGCGCG	TCAGCGGGTG	120
TTGGCGGGTG	TCGGGGCTGG	CTTAACTATG	CGGCATCAGA	GCAGATTGTA	CTGAGAGTGC	180
ACCATATGCG	GTGTGAAATA	CCGCACAGAT	GCGTAAGGAG	AAAATACCGC	ATCAGATTGG	240
CTATTGGCCA	TTGCATACGT	TGTATCCATA	TCATAATATG	TACATTTATA	TTGGCTCATG	300
TCCAACATTA	CCGCCATGTT	GACATTGATT	ATTGACTAGT	TATTAATAGT	AATCAATTAC	360
GGGGTCATTA	GTTCATAGCC	CATATATGGA	GTTCCGCGTT	ACATAACTTA	CGGTAAATGG	420
CCCGCCTGGC	TGACCGCCCA	ACGACCCCCG	CCCATTGACG	TCAATAATGA	CGTATGTTCC	480
CATAGTAACG	CCAATAGGGA	CTTTCCATTG	ACGTCAATGG	GTGGAGTATT	TACGGTAAAC	540
TGCCCACTTG	GCAGTACATC	AAGTGTATCA	TATGCCAAGT	ACGCCCCTA	TTGACGTCAA	600
TGACGGTAAA	TGGCCCGCCT	GGCATTATGC	CCAGTACATG	ACCTTATGGG	ACTTTCCTAC	660
TTGGCAGTAC	ATCTACGTAT	TAGTCATCGC	TATTACCATG	GTGATGCGGT	TTTGGCAGTA	720
CATCAATGGG	CGTGGATAGC	GGTTTGACTC	ACGGGGATTT	CCAAGTCTCC	ACCCCATTGA	780
CGTCAATGGG	AGTTTGTTTT	GGCACCAAAA	TCAACGGGAC	TTTCCAAAAT	GTCGTAACAA	840
CTCCGCCCCA	TTGACGCAAA	TGGGCGGTAG	GCGTGTACGG	TGGGAGGTCT	ATATAAGCAG	900
AGCTCGTTTA	GTGAACCGTC	AGATCGCCTG	GAGACGCCAT	CCACGCTGTT	TTGACCTCCA	960
TAGAAGACAC	CGGGACCGAT	CCAGCCTCCG	CGGCCGGGAA	CGGTGCATTG	GAACGCGGAT	1020
TCCCCCTCCC	AAGAGTGACG	TAAGTACCGC	CTATAGAGTC	TATAGGCCCA	CCCCCTTGGC	1080
TTCTTATCCA	TCCTATACTG	TTTTTGGCTT	GGGGTCTATA	CACCCCCGCT	TCCTCATGTT	1140
ATACCTCATC	CTATACCTTA	GCCTATAGGT	GTGGGTTATT	GACCATTATT	GACCACTCCC	1200
CTATTCCTCA	CCATACTTTC	CATTACTAAT	CCATAACATG	GCTCTTTGCC	ACAACTCTCT	1260
TTATIGGIGA	TATCCCAATA	CACTGTCCTT	CAGAGACTGA	CACGGACTCT	GTATTTTTAC	1320
ACCAMCCCCCM	CTCATTTATT	ATTTACAAAT	TCACATATAC	AACACCACCG	TCCCCAGTGC	1380
AGGAIGGGGI	CICATILATI	AACGTGGGAT	CTCCACGCGA	ATCTCGGGTA	CGTGTTCCGG	1440
A CAMCCCCCTC	TATTAAACAT	GCGGCGGAGC	TTCTACATCC	CACCCCTCCT	CCCATGCCTC	1500
CACCCACTC	TICICCGGIA	GCAGCTCCTT	CCTCCTAACA	CTGGAGGCCA	GACTTAGGCA	1560
CAGCGACTCA	CCCACCACCA	CCAGTGTGCC	CCACAAGGCC	CTCCCCCTAC	GGTATGTGTC	1620
CAGCACGATG	CCCACCACCA	GGGCTTGCAC	CCCTCACCCA	TTTCCAACAC	TTAAGGCAGC	1680
TGAAAATGAG	CICGGGGAGC	GCTGAGTTGT	TCTCTTCTCA	TAAGAGTCAG	AGGTAACTCC	1740
GGCAGAAGAA	CMCMMA A CCC	TGGAGGGCAG	TOTALTCIGA	CCACTACTCC	TTGCTGCCGC	1800
CGTTGCGGTG	CIGITAACGG	GCTGACAGAC	TAACACACTC	TTCCTTTTCCA	TGGGTCTTTT	1860
GCGCGCCACC	AGACATAATA	TCTGCTGTGC	COUNCES	CCACCCATCT	CTTCTTTCCC	1920
CTGCAGTCAC	CGTCCTTAGA	ACCCTGGAAG	CTICIAGIIG	CACTCTCCTT	TCCTAATAAA	1980
CCTCCCCCGT	GCCTTCCTTG	TGTCTGAGTA	CCCCCCCCCCC	TATTCTCCCC	CCTCCCCTCC	2040
ATGAGGAAAT	TGCATCGCAT	TGTCTGAGTA	GGTGTCATTC	CCAMCCMCCC	CATCCCCTCC	2100
GGCAGCACAG	CAAGGGGGAG	GATTGGGAAG	ACAATAGCAG	CMCCMCCCCC	ACAAACAACC	2160
GCTCTATGGG	TACCCAGGTG	CTGAAGAATT	GACCCGGTTC	CTCCTGGGCC	CULCCACCCC	2220
AGGCACATCC	CCTTCTCTGT	GACACACCCT	GTCCACGCCC	AAMCCCACCC	CCTAAACTAC	2280
CACTCATAGG	ACACTCATAG	CTCAGGAGGG	CICCGCCTTC	AATCCCACCC	CCAACACTCC	2340
TTGGAGCGGT	CTCTCCCTCC	CTCATCAGCC	CACCAAACCA	AACCTAGCCT	CCAAGAGIGG	2400
GAAGAAATTA	AAGCAAGATA	GGCTATTAAG	TGCAGAGGGA	GAGAAAATGC	CTCCAACATG	2460
TGAGGAAGTA	ATGAGAGAAA	TCATAGAATT	TCTTCCGCTT	CCTCGCTCAC	1GACTCGCTG	2520
CGCTCGGTCG	TTCGGCTGCG	GCGAGCGGTA	TCAGCTCACT	CAAAGGCGGT	AATACGGTTA	2520
TCCACAGAAT	CAGGGGATAA	CGCAGGAAAG	AACATGTGAG	CAAAAGGCCA	GCAAAAGGCC	2640
AGGAACCGTA	AAAAGGCCGC	GTTGCTGGCG	TTTTTCCATA	GGCTCCGCCC	CCCTGACGAG	2700
CATCACAAAA	ATCGACGCTC	AAGTCAGAGG	TGGCGAAACC	CGACAGGACT	ATAAAGATAC	2760
CAGGCGTTTC	CCCCTGGAAG	CTCCCTCGTG	CGCTCTCCTG	TTCCGACCCT	GCCGCTTACC	
GGATACCTGT	CCGCCTTTCT	CCCTTCGGGA	AGCGTGGCGC	TTTCTCAATG	CTCACGCTGT	2820
AGGTATCTCA	GTTCGGTGTA	GGTCGTTCGC	TCCAAGCTGG	GCTGTGTGCA	CGAACCCCCC	2880
GTTCAGCCCG	ACCGCTGCGC	CTTATCCGGT	AACTATCGTC	TTGAGTCCAA	CCCGGTAAGA	2940
CACGACTTAT	CGCCACTGGC	AGCAGCCACT	GGTAACAGGA	TTAGCAGAGC	GAGGTATGTA	3000
GGCGGTGCTA	CAGAGTTCTT	GAAGTGGTGG	CCTAACTACG	GCTACACTAG	AAGGACAGTA	3060
TTTGGTATCT	GCGCTCTGCT	GAAGCCAGTT	ACCTTCGGAA	AAAGAGTTGG	TAGCTCTTGA	3120
TCCGGCAAAC	AAACCACCGC	TGGTAGCGGT	GGTTTTTTTG	TTTGCAAGCA	GCAGATTACG	3180

			тта в таптат	CTACGGGGTC	TGACGCTCAG	3240
CGCAGAAAAA		AGAAGATCCT	TTGATCTTTT	TATCAAAAAG	GATCTTCACC	3300
100:11:00:11:1	ACTCACGTTA	AGGGATTTTG	GTCATGAGAT	AAAGTATATA	TGAGTAAACT	3360
TAGATCCTTT	TAAATTAAAA	ATGAAGTTTT	AAATCAATCT		CTGTCTATTT	3420
TGGTCTGACA	GTTACCAATG	CTTAATCAGT	GAGGCACCTA	TCTCAGCGAT	CTCGTGAAGA	3480
CGTTCATCCA	TAGTTGCCTG	ACTCCGGGGG	GGGGGGGCGC	TGAGGTCTGC	AAGTGAGGGA	3540
AGGTGTTGCT	GACTCATACC	AGGCCTGAAT	CGCCCCATCA	TCCAGCCAGA		3600
GCCACGGTTG	ATGAGAGCTT	TGTTGTAGGT	GGACCAGTTG	GTGATTTTGA	ACTTTTGCTT	3660
TGCCACGGAA	CGGTCTGCGT	TGTCGGGAAG	ATGCGTGATC	TGATCCTTCA	ACTCAGCAAA	3720
AGTTCGATTT	ATTCAACAAA	GCCGCCGTCC	CGTCAAGTCA	GCGTAATGCT	CTGCCAGTGT	
TACAACCAAT	TAACCAATTC	TGATTAGAAA	AACTCATCGA	GCATCAAATG	AAACTGCAAT	3780
TTATTCATAT	CAGGATTATC	AATACCATAT	TTTTGAAAAA	GCCGTTTCTG	TAATGAAGGA	3840
GAAAACTCAC	CGAGGCAGTT	CCATAGGATG	GCAAGATCCT	GGTATCGGTC	TGCGATTCCG	3900
ACTCGTCCAA	CATCAATACA	ACCTATTAAT	TTCCCCTCGT	CAAAAATAAG	GTTATCAAGT	3960
GAGAAATCAC	CATGAGTGAC	GACTGAATCC	GGTGAGAATG	GCAAAAGCTT	ATGCATTTCT	4020
TTCCAGACTT	GTTCAACAGG	CCAGCCATTA	CGCTCGTCAT	CAAAATCACT	CGCATCAACC	4080
AAACCGTTAT	TCATTCGTGA	TTGCGCCTGA	GCGAGACGAA	ATACGCGATC	GCTGTTAAAA	4140
GGACAATTAC	AAACAGGAAT	CGAATGCAAC	CGGCGCAGGA	ACACTGCCAG	CGCATCAACA	4200
ATATTTTCAC	CTGAATCAGG	ATATTCTTCT	AATACCTGGA	ATGCTGTTTT	CCCGGGGATC	4260
GCAGTGGTGA	GTAACCATGC	ATCATCAGGA	GTACGGATAA	AATGCTTGAT	GGTCGGAAGA	4320
GGCATAAATT	CCGTCAGCCA	GTTTAGTCTG	ACCATCTCAT	CTGTAACATC	ATTGGCAACG	4380
CTACCTTTGC	CATGTTTCAG	AAACAACTCT	GGCGCATCGG	GCTTCCCATA	CAATCGATAG	4440
ATTGTCGCAC	CTGATTGCCC	GACATTATCG	CGAGCCCATT	TATACCCATA	TAAATCAGCA	4500
TCCATGTTGG	AATTTAATCG	CGGCCTCGAG	CAAGACGTTT	CCCGTTGAAT	ATGGCTCATA	4560
ACACCCCTTG	TATTACTGTT	TATGTAAGCA	GACAGTTTTA	TTGTTCATGA	TGATATATTT	4620
TTATCTTGTG	CAATGTAACA	TCAGAGATTT	TGAGACACAA	CGTGGCTTTC	CCCCCCCCC	4680
CATTATTGAA		GGGTTATTGT	CTCATGAGCG	GATACATATT	TGAATGTATT	4740
Q111 1111 1 Q1	AACAAATAGG	GGTTCCGCGC	ACATTTCCCC	GAAAAGTGCC	ACCTGACGTC	4800
TAAGAAACCA		GACATTAACC	TATAAAAATA	GGCGTATCAC	GAGGCCCTTT	4860
CGTC	IIAIIAICAI	0				4864
CGIC						

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 15 base pairs
 (B) TYPE: nucleic acid

 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

AGCAGAAGCA GAGCA

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 base pairs
 - (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
TCACCGTCCT TAGATCAAGC AGGGTTAATA ATCACTCACT GAGTGACATC AAAATCATGG CGTCCCAAGG CACCAAACGG TCTTATGAAC AGATGGAAAC TGATGGGGAA CGCCAGATT	60 119
(2) INFORMATION FOR SEQ ID NO:21:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 67 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GAGGGGCAAA CAACAGATGG CTGGCAACTA GAAGGCACAG CAGATATTTT TTCCTTAATT GTCGTAC	60 67
(2) INFORMATION FOR SEQ ID NO:22:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 15 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
AGCAGAAGCA CGCAC	15
(2) INFORMATION FOR SEQ ID NO:23:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 15 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
AGCAGAAGCA CAGCA	15

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
CCTTAGATCG GAAATAAAAA CAACCAAAAT GAA	33
(2) INFORMATION FOR SEQ ID NO:25:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
GCAGATCCTT ATATTTCTGA AATTCTGGTC TCAGAT	36
(2) INFORMATION FOR SEQ ID NO:26:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 102 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
ACCGTCCTTA GATCCAGAAG CAGAGCATTT TCTAATATCC ACAAAATGAA GGCAATAATT GTACTACTCA TGGTAGTAAC ATCCAACGCA GATCGAATCT GC	60 102
(2) INFORMATION FOR SEQ ID NO:27:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 42 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: double(D) TOPOLOGY: both	

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
GGCACAGCAG ATCTTTCAAT AACGTTTCTT TGTAATGGTA AC	42
(2) INFORMATION FOR SEQ ID NO:28:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
CTAACAGACT GTTCCTTTCC ATG	23
(2) INFORMATION FOR SEQ ID NO:29:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: YES (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GGAGTGGCAC CTTCCAGG	18
(2) INFORMATION FOR SEQ ID NO:30:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 12 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
AGCAAAAGCA GG	12

	(2) INFORMATION FOR SEQ ID NO:31:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 14 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
AGCA	GAAGCG GAGC	14
	(2) INFORMATION FOR SEQ ID NO:32:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 35 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:	
CCAC	ATGTCG ACCCGTAAAA AGGCCGCGTT GCTGG	35
	(2) INFORMATION FOR SEQ ID NO:33:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GGTA	CAACCA TGAAGACTAT CATTGCTTTG AGC	33
	(2) INFORMATION FOR SEQ ID NO:34:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 37 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
CCACATAGAT CTTCAAATGC AAATGTTGCA CCTAATG 3
(2) INFORMATION FOR SEQ ID NO:35:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
GGTACAACCA TGAAAGCAAA ACTACTAGTC CTGTTATG
(2) INFORMATION FOR SEQ ID NO:36:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 32 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
CCACATTCAG ATGCATATTC TACACTGCAA AG 33
(2) INFORMATION FOR SEQ ID NO:37:
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGTACAACCA TGAAGGCAAT AATTGTACTA CTCATG	36
(2) INFORMATION FOR SEQ ID NO:38:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:	
CCACATTTAT AGACAGATGG AGCAAGAAAC ATTGTC	36
(2) INFORMATION FOR SEQ ID NO:39:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
GGTACAAGAT CTACCATGCT TCTAACCGAG GTC	33
(2) INFORMATION FOR SEQ ID NO:40:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
CCACATAGAT CTTCACTTGA ACCGTTGCAT CTGCAC	36
(2) INFORMATION FOR SEQ ID NO:41:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid	

(C) STRANDEDNESS: both (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
GGTACAGGAT CCACCATGTC CAACATGGAT ATTGACGGC	39
(2) INFORMATION FOR SEQ ID NO:42:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 39 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
CCACATGGAT CCTTAATAAT CGAGGTCATC ATAATCCTC	39
(2) INFORMATION FOR SEQ ID NO:43:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 42 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
GGTACAGGAT CCACCATGTC GCTGTTTGGA GACACAATTG CC	42
(2) INFORMATION FOR SEQ ID NO:44:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: linear	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

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CCACATGGAT CCTTATAGGT ATTTCTTCAC AAGAGCTG

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 3553 base pairs(B) TYPE: nucleic acid

 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (iii) HYPOTHETICAL: NO
- (iv) ANTISENSE: NO
- (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

				ATAATATGTA		60
GGCTCATGTC	CAACATTACC			TGACTAGTTA		120
TCAATTACGG	GGTCATTAGT	TCATAGCCCA	TATATGGAGT	TCCGCGTTAC	ATAACTTACG	180
GTAAATGGCC	CGCCTGGCTG	ACCGCCCAAC	GACCCCCGCC	CATTGACGTC	AATAATGACG	240
		AATAGGGACT			GGAGTATTTA	300
			GTGTATCATA		GCCCCCTATT	360
			CATTATGCCC		CTTATGGGAC	420
TTTCCTACTT	GGCAGTACAT	CTACGTATTA	GTCATCGCTA		GATGCGGTTT	480
	TCAATGGGCG				AAGTCTCCAC	540
			CACCAAAATC		TCCAAAATGT	600
			GGCGGTAGGC		GGAGGTCTAT	660
				GACGCCATCC		720
GACCTCCATA				GCCGGGAACG		780
ACGCGGATTC	CCCGTGCCAA	GAGTGACGTA	AGTACCGCCT	ATAGAGTCTA	TAGGCCCACC	840
CCCTTGGCTT	CTTATGCATG	CTATACTGTT	TTTGGCTTGG	GGTCTATACA	CCCCCGCTTC	900
				GGGTTATTGA	CCATTATTGA	960
CCACTCCCCT	ATTGGTGACG	ATACTTTCCA	TTACTAATCC	ATAACATGGC	TCTTTGCCAC	1020
AACTCTCTTT	ATTGGCTATA	TGCCAATACA	CTGTCCTTCA	GAGACTGACA	CGGACTCTGT	1080
	GATGGGGTCT			ACATATACAA		1140
				TCTCCACGCG		1200
				CTTCTACATC	CGAGCCCTGC	1260
TCCCATGCCT	CCAGCGACTC	ATGGTCGCTC	GGCAGCTCCT	TGCTCCTAAC	AGTGGAGGCC	1320
AGACTTAGGC	ACAGCACGAT	GCCCACCACC	ACCAGTGTGC	CGCACAAGGC	CGTGGCGGTA	1380
			CGGGCTTGCA		ATTTGGAAGA	1440
			AGCTGAGTTG		ATAAGAGTCA	1500
			GTGGAGGGCA		AGCAGTACTC	1560
GTTGCTGCCG	CGCGCGCCAC	CAGACATAAT	AGCTGACAGA	CTAACAGACT	GTTCCTTTCC	1620
ATGGGTCTTT			ATCTGCTGTG		GCCAGCCATC	1680
TGTTGTTTGC	CCCTCCCCCG	TGCCTTCCTT	GACCCTGGAA	GGTGCCACTC	CCACTGTCCT	1740
			TTGTCTGAGT		CTATTCTGGG	1800
				GACAATAGCA	GGCATGCTGG	1860
			AGCGGCCGTA		GAAGAATTGA	1920
			TTGCTGGCGT		GCTCCGCCCC	1980
CCTGACGAGC	ATCACAAAAA	TCGACGCTCA		GGCGAAACCC	GACAGGACTA	2040
TAAAGATACC	AGGCGTTTCC	CCCTGGAAGC		GCTCTCCTGT	TCCGACCCTG	2100
	GATACCTGTC		CCTTCGGGAA		TTCTCAATGC	2160
TCACGCTGTA	GGTATCTCAG		GTCGTTCGCT		CTGTGTGCAC	2220
	TTCAGCCCGA		TTATCCGGTA		TGAGTCCAAC	2280
	ACGACTTATC		GCAGCCACTG		TAGCAGAGCG	2340
		AGAGTTCTTG		CTAACTACGG	CTACACTAGC	2400
TGAAGGACAG	TATTTGGTAT	CTGCGCTCTG	CTGAAGCCAG	TTACCTTCGG	AAAAAGAGTT	2460

GGTAGCTCTT GATCCGGCAA ACAAACCACC GCTGGTAGCG GTGGTTTTTT TGTTTGCAAG CAGCAGATTA CGCGCAGAAA AAAAGGATCT CAAGAAGATC CTTTGATCAT TTCTACGTGA AAAACCACC GAGCATCAAA TGAAACTGCA ATTTATTCAT ATCAGGATTA TCAATACCAT TTTTTGAAA ACCCGTTTC TGTAATGAAG GAGAAAACTC ACCGAGGCAG TTCCATAGGA TGGCAAGAAT ACGACTGATC CTTTCCAGAC TTATGCATT CTTTCCAGAC TTTTCAACA ACCATGAGT ACCATGAGAAATCA ACCATGAGT ACCATGAGAAATCA CCAACCGTT ATCAAAATCA CTCGCATCAA AAGGACAATT ACAAACAGA ATTGCACT TTCCCGTGCA TCCCGCATCAA AAAATGCTTG AGCGCATCAA AAAATGCTTG ATCGCATCAA ACCATGAGT ACCATGAGT ACCATGATCA ACCATGAGT ACCATGATCA ACCAGCAT TACCGCTCGAAAATCA CCAAAACCGTT ATCATTCCT GAATACCAT TTCCCGTGAA ACGACTGATC ACCAGAAACCGT ATCATTCCT GAATACCAT TCCCGTCGAAAATCA CCAAAACCGT ATCATTCTT CTAATACCTG GAATGCTGT TTCCCGGGGA ACCGCACTAA ACGACCATAAA TCCCTGAATCA GGATATTCTT CTAATACCTG GAATGCTACA ACGGCGCAGA ACCGGCGAAAAAAAAATGCTTG ATCATTGGCAA GAGCACTAAAA TTCCCGTCAGC CAGTTTAGTC TGACCATCAC GAGCACTACA ACGACCATT ACAAACAGAAACCAT GCATCATCAG GAGTACCAT TGACCATCTC ACCATGATCA ACCGCCGAACAAAAAAAATGCTTG ACCATGATAAAATCAG CACTGATTC ACCATGATCA GAAACAACT TGACCATCTC ACAATCATCA GAGAACAACT CTGGCGCATC ACCATGATT ACCCTTTT GCCATTTC AGAAACAACT CTGGCGCATC ACCATGATT ACCCTTTT GCCATTTC AGAAACAACT CTGGCGCATC ACCTGATTAC CCGACCCAT TTTTATACCCA TATAAAATCAG CATCCATGTT GCCATTTTC CCGACCATCA ACCTGATTAC CAGCAGACCT TTTTATACCCA TATAAAATCAG CATCCATGTT GACAATCAT TTTTTATCTTG TTTTATCTTG TTTTATGTAAA CACCCCT TTTTATTACTG TTTTATGTAAG CAGAACAACT TTTTATGTAAAAAAAAAA	2520 2580 2640 2700 2760 2820 2880 2940 3060 3120 3180 3340 3360 3420 3553
(2) INFORMATION FOR SEQ ID NO:46:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 72 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: CDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
TCACCGTCCT TAGATCGGTA CAACCATGAA GACTATCATT GCTTTGAGCT ACATTTTATG TCTGGTTTTC GC	60 72
(2) INFORMATION FOR SEQ ID NO:47:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 111 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
TCATGCTTTT TGCTTTGTGT TGTTTTGCTG GGGTTCATCA TGTGGGCCTG CCAAAAAGGC AACATTAGGT GCAACATTTG CATTTGAAGA TCTATGTGGG ATCTGCTGTG C	60 111
(2) INFORMATION FOR SEQ ID NO:48:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 63 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
TTAGATCGGA ACATGAAAGC AAAACTACTA GTCCTGTTAT GTGCATTTAC AGCTACATAT GCA	60 63
(2) INFORMATION FOR SEQ ID NO:49:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 102 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: both 	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:	
CTGGTGCTTT TGGTCTCCCT GGGGGCAATC AGCTTCTGGA TGTGTTCTAA TGGGTCTTTG CAGTGTAGAA TATGCATCTG AATGTGGGAT CTGCTGTGCC TT	60 102
(2) INFORMATION FOR SEQ ID NO:50:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 108 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:	
CCTTAGATCG GTACAACCAT GAAGGCAATA ATTGTACTAC TCATGGTAGT AACATCCAAC GCAGATCGAA TCTGCACTGG GATAACATCT TCAAACTCAC CTCATGTG	60 108
(2) INFORMATION FOR SEQ ID NO:51:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 102 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA	

(iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
TTGGCTGTAA CATTGATGAT AGCTATTTTT ATTGTTTATA TGGTCTCCAG AGACAATGTT TCTTGCTCCA TCTGTCTATA AATGTGGGAT CTGCTGTGCC TT	60 102
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 84 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
GTCCTTAGAT CCACCATGGC GTCCCAAGGC ACCAAACGGT CTTATGAACA GATGGAAACT GATGGGGAAC GCCAGAATGC AACT	60 84
(2) INFORMATION FOR SEQ ID NO:53:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 108 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
GAAAAGGCAA CGAACCCGAT CGTGCCCTCT TTTGACATGA GTAATGAAGG ATCTTATTTC TTCGGAGACA ATGCAGAAGA GTACGACAAT TAAGGATCTG CTGTGCCT	60 108
(2) INFORMATION FOR SEQ ID NO:54:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 132 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	

(xi)	SEQUENCE D	ESCRIPTION:	SEQ ID NO:	54:		
	GCCCCTCAA	GAGTCTTCTA AGCCGAAATC				60 120 132
(2	2) INFORMAT	ION FOR SEQ	ID NO:55:			
(A) (B) (C)		ESS: both				
(iii) (iv) (v) E	MOLECULE T HYPOTHETI ANTISENSE: FRAGMENT TY ORIGINAL S	CAL: NO NO PE:				
(xi)	SEQUENCE D	ESCRIPTION:	SEQ ID NO:5	55:		
		TACTGGTCTA GCAGATGCAA				60 120 129
(2	?) INFORMAT	ION FOR SEQ	ID NO:56:			
(A) (B) (C)		ESS: both				
(iii) (iv) (v) F	MOLECULE T HYPOTHETIC ANTISENSE: RAGMENT TY ORIGINAL SO	CAL: NO NO PE:				
(xi)	SEQUENCE D	ESCRIPTION:	SEQ ID NO:5	66:		
CTTAGATCCA ACACCGGAAG		CATGGATATT T	GACGGTATCA	ACACTGGGAC	AATTGACAAA	60 81
(2) INFORMAT	ION FOR SEQ	ID NO:57:			
(A) (B) (C)		ESS: both				
(iii) (iv) (v) F	MOLECULE TO HYPOTHETIC ANTISENSE: 'RAGMENT TYPO ORIGINAL SO	CAL: NO NO PE:				
(xi)	SEQUENCE DI	ESCRIPTION:	SEQ ID NO:5	57:		

GTTGAAATTC CAATTAAGCA GACCATCCCC AATTTCTTCT TTGGGAGGGA CACAGCAGAG 60

GATTATGATG ACCTCGATTA TTAAGGATCT GCTGTG	96
(2) INFORMATION FOR SEQ ID NO:58:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 96 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:	
CTTAGATCCA CCATGTCGCT GTTTGGAGAC ACAATTGCCT ACCTGCTTTC ATTGACAGAA GATGGAGAAG GCAAAGCAGA ACTAGCAGAA AAATTA	60 96
(2) INFORMATION FOR SEQ ID NO:59:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 123 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:	
AGATCTCTTG GGGCAAGTCA AGAGAATGGG GAAGGAATTG CAAAGGATGT GATGGAAGTG CTAAAGCAGA GCTCTATGGG AAATTCAGCT CTTGTGAAGA AATACCTATA AGGATCTGCT GTG	60 120 123
(2) INFORMATION FOR SEQ ID NO:60:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 33 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
GGTACAAATA TTGGCTATTG GCCATTGCAT ACG	33
(2) INFORMATION FOR SEQ ID NO:61:	
(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 36 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
CCACATCTCG AGGAACCGGG TCAATTCTTC AGCACC	36
(2) INFORMATION FOR SEQ ID NO:62:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 38 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
GGTACAGATA TCGGAAAGCC ACGTTGTGTC TCAAAATC	38
(2) INFORMATION FOR SEQ ID NO:63:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 37 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: both(D) TOPOLOGY: both	
<pre>(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO (iv) ANTISENSE: NO (v) FRAGMENT TYPE: (vi) ORIGINAL SOURCE:</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
CCACATGGAT CCGTAATGCT CTGCCAGTGT TACAACC	37
(2) INFORMATION FOR SEQ ID NO:64:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: both (D) TOPOLOGY: both 	
(ii) MOLECULE TYPE: cDNA (iii) HYPOTHETICAL: NO	

- (v) FRAGMENT TYPE:
 (vi) ORIGINAL SOURCE:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

GGTACATGAT CACGTAGAAA AGATCAAAGG ATCTTCTTG

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